

74251seq

SEQUENCE LISTING

<110> Boehringer Ingelheim International GmbH

<120> Tumour-expressed polypeptide B345

<130> case12_214

<140>

<141>

<160> 35

<170> PatentIn Ver. 2.1

<210> 1

<211> 5896

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)..(214)

<220>

<221> CDS

<222> (215)..(2464)

<220>

<221> 3'UTR

<222> (2465)..(5896)

<400> 1

cttgagatat tagaattcgc gactcctgaa ctgcggggc tctatcgac tgctaggggt 60

tctgctgctg ggtgcggcgc gcctgcgcgc cggggcagaa gcttttgaga ttgctctgcc 120

acgagaaagc aacattacag ttctcataaa gctggggacc ccgactctgc tggcaaaacc 180

ctgttacatc gtcatttcta aaagacatat aacc atg ttg tcc atc aag tct gga 235

Met Leu Ser Ile Lys Ser Gly

1

5

gaa aga ata gtc ttt acc ttt agc tgc cag agt oct gag aat cac ttt 283

Glu Arg Ile Val Phe Thr Phe Ser Cys Gln Ser Pro Glu Asn His Phe

10

15

20

gtc ata gag atc cag aaa aat att gac tgt atg tca ggc cca tgt oct 331

Val Ile Glu Ile Gln Lys Asn Ile Asp Cys Met Ser Gly Pro Cys Pro

25

30

35

ttt ggg gag gtt cag ctt cag ccc tog aca tog ttg ttg cct acc ctc 379

Phe Gly Glu Val Gln Leu Gln Pro Ser Thr Ser Leu Leu Pro Thr Leu

40

45

50

55

aac aga act ttc atc tgg gat gtc aaa gct cat aag agc atc ggt tta	427
Asn Arg Thr Phe Ile Trp Asp Val Lys Ala His Lys Ser Ile Gly Leu	
60 65 70	
gag ctg cag ttt tcc atc cct cgc ctg agg cag atc ggt ccg ggt gag	475
Glu Leu Gln Phe Ser Ile Pro Arg Leu Arg Gln Ile Gly Pro Gly Glu	
75 80 85	
agc tgc cca gac gga gtc act cac tcc atc agc ggc cga atc gat gcc	523
Ser Cys Pro Asp Gly Val Thr His Ser Ile Ser Gly Arg Ile Asp Ala	
90 95 100	
acc gtg gtc agg atc gga acc ttc tgc agc aat ggc act gtg tcc cgg	571
Thr Val Val Arg Ile Gly Thr Phe Cys Ser Asn Gly Thr Val Ser Arg	
105 110 115	
atc aag atg caa gaa gga gtg aaa atg gcc tta cac ctc cca tgg ttc	619
Ile Lys Met Gln Glu Gly Val Lys Met Ala Leu His Leu Pro Trp Phe	
120 125 130 135	
cac ccc aga aat gtc tcc ggc ttc agc att gca aac cgc tca tct ata	667
His Pro Arg Asn Val Ser Gly Phe Ser Ile Ala Asn Arg Ser Ser Ile	
140 145 150	
aaa cgt ctg tgc atc atc gag tct gtg ttt gag ggt gaa ggc tca gca	715
Lys Arg Leu Cys Ile Ile Glu Ser Val Phe Glu Gly Glu Gly Ser Ala	
155 160 165	
acc ctg atg tct gcc aac tac oca gaa ggc ttc cct gag gat gag ctc	763
Thr Leu Met Ser Ala Asn Tyr Pro Glu Gly Phe Pro Glu Asp Glu Leu	
170 175 180	
atg acg tgg cag ttt gtc gtt oct gca cac ctg cgg gcc agc gtc tcc	811
Met Thr Trp Gln Phe Val Val Pro Ala His Leu Arg Ala Ser Val Ser	
185 190 195	
ttc ctc aac ttc aac ctc tcc aac tgt gag agg aag gag gag cgg gtt	859
Phe Leu Asn Phe Asn Leu Ser Asn Cys Glu Arg Lys Glu Glu Arg Val	
200 205 210 215	
gaa tac tac atc ccg ggc tcc acc acc aac ccc gag gtg ttc aag ctg	907
Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro Glu Val Phe Lys Leu	
220 225 230	
gag gac aag cag cct ggg aac atg gcg ggg aac ttc aac ctc tct ctg	955
Glu Asp Lys Gln Pro Gly Asn Met Ala Gly Asn Phe Asn Leu Ser Leu	
235 240 245	
caa ggc tgt gac caa gat gcc caa agt cca ggg atc ctc cgg ctg cag	1003
Gln Gly Cys Asp Gln Asp Ala Gln Ser Pro Gly Ile Leu Arg Leu Gln	
250 255 260	
ttc caa gtt ttg gtc caa cat cca caa aat gaa agc aat aaa atc tac	1051
Phe Gln Val Leu Val Gln His Pro Gln Asn Glu Ser Asn Lys Ile Tyr	
265 270 275	

gtg gtt gac ttg agt aat gag oga gcc atg tca ctc acc atc gag cca	1099
Val Val Asp Leu Ser Asn Glu Arg Ala Met Ser Leu Thr Ile Glu Pro	
280 285 290 295	
ogg ccc gtc aaa cag agc cgc aag ttt gtc cct ggc tgt ttc gtg tgt	1147
Arg Pro Val Lys Gln Ser Arg Lys Phe Val Pro Gly Cys Phe Val Cys	
300 305 310	
cta gaa tct ogg acc tgc agt agc aac ctc acc ctg aca tct ggc tcc	1195
Leu Glu Ser Arg Thr Cys Ser Ser Asn Leu Thr Leu Thr Ser Gly Ser	
315 320 325	
aaa cac aaa atc tcc ttc ctt tgt gat gat ctg aca cgt ctg tgg atg	1243
Lys His Lys Ile Ser Phe Leu Cys Asp Asp Leu Thr Arg Leu Trp Met	
330 335 340	
aat gtg gaa aaa acc ata agc tgc aca gac cac ogg tac tgc caa agg	1291
Asn Val Glu Lys Thr Ile Ser Cys Thr Asp His Arg Tyr Cys Gln Arg	
345 350 355	
aaa tcc tac tca ctc cag gtg ccc agt gac atc ctc cac ctg cct gtg	1339
Lys Ser Tyr Ser Leu Gln Val Pro Ser Asp Ile Leu His Leu Pro Val	
360 365 370 375	
gag ctg cat gac ttc tcc tgg aag ctg ctg gtg ccc aag gac agg ctc	1387
Glu Leu His Asp Phe Ser Trp Lys Leu Val Pro Lys Asp Arg Leu	
380 385 390	
agc ctg gtg ctg gtg cca gcc cag aag ctg cag cag cat aca cac gag	1435
Ser Leu Val Leu Val Pro Ala Gln Lys Leu Gln Gln His Thr His Glu	
395 400 405	
aag ccc tgc aac acc agc ttc agc tac ctc gtg gcc agt gcc ata ccc	1483
Lys Pro Cys Asn Thr Ser Phe Ser Tyr Leu Val Ala Ser Ala Ile Pro	
410 415 420	
agc cag gac ctg tac ttc ggc tcc ttc tgc ccg gga ggc tct atc aag	1531
Ser Gln Asp Leu Tyr Phe Gly Ser Phe Cys Pro Gly Gly Ser Ile Lys	
425 430 435	
cag atc cag gtg aag cag aac atc tgg gtg acc ctt cgc acc ttt gcc	1579
Gln Ile Gln Val Lys Gln Asn Ile Ser Val Thr Leu Arg Thr Phe Ala	
440 445 450 455	
ccc agc ttc caa caa gag gcc tcc agg cag ggt ctg acg gtg tcc ttt	1627
Pro Ser Phe Gln Gln Glu Ala Ser Arg Gln Gly Leu Thr Val Ser Phe	-
460 465 470	
ata cct tat ttc aaa gag gaa ggc gtt ttc acg gtg acc cct gac aca	1675
Ile Pro Tyr Phe Lys Glu Glu Gly Val Phe Thr Val Thr Pro Asp Thr	
475 480 485	
aaa agc aag gtc tac ctg agg acc ccc aac tgg gac cgg ggc ctg cca	1723
Lys Ser Lys Val Tyr Leu Arg Thr Pro Asn Trp Asp Arg Gly Leu Pro	
490 495 500	

tcc ctc acc tct gtg tcc tgg aac atc agc gtg ccc aga gac cag gtg Ser Leu Thr Ser Val Ser Trp Asn Ile Ser Val Pro Arg Asp Gln Val 505 510 515	1771
gcc tgc ctg act ttc ttt aag gag cgg agc ggc gtg gtc tgc cag aca Ala Cys Leu Thr Phe Phe Lys Glu Arg Ser Gly Val Val Cys Gln Thr 520 525 530 535	1819
ggg cgc gca ttc atg atc atc cag gag cag cgg acc cgg gct gag gag Gly Arg Ala Phe Met Ile Ile Gln Glu Gln Arg Thr Arg Ala Glu Glu 540 545 550	1867
atc ttc agc ctg gac gag gat gtg ctc ccc aag cca agc ttc cac cat Ile Phe Ser Leu Asp Glu Asp Val Leu Pro Lys Pro Ser Phe His His 555 560 565	1915
cac agc ttc tgg gtc aac atc tct aac tgc agc ccc acg agc ggc aag His Ser Phe Trp Val Asn Ile Ser Asn Cys Ser Pro Thr Ser Gly Lys 570 575 580	1963
cag cta gac ctg ctc ttc tgg gtg aca ctt acc cca agg act gtg gac Gln Leu Asp Leu Leu Phe Ser Val Thr Leu Thr Pro Arg Thr Val Asp 585 590 595	2011
ttg act gtc atc ctc atc gca gcg gtg gga ggt gga gtc tta ctg ctg Leu Thr Val Ile Leu Ile Ala Ala Val Gly Gly Gly Val Leu Leu Leu 600 605 610 615	2059
tct gcc ctc ggg ctc atc att tgc tgt gtg aaa aag aag aaa aag aag Ser Ala Leu Gly Leu Ile Ile Cys Cys Val Lys Lys Lys Lys Lys Lys 620 625 630	2107
aca aac aag ggc ccc gct gtg ggt atc tac aat ggc aac atc aat act Thr Asn Lys Gly Pro Ala Val Gly Ile Tyr Asn Gly Asn Ile Asn Thr 635 640 645	2155
gag atg cca ggc agc caa aaa agt ttc aga aag ggc gaa agg aca atg Glu Met Pro Gly Ser Gln Lys Ser Phe Arg Lys Gly Glu Arg Thr Met 650 655 660	2203
act ccc atg tgt atg cag tca tgg agg aca cca tgg tat atg ggc atc Thr Pro Met Cys Met Gln Ser Ser Arg Thr Pro Trp Tyr Met Gly Ile 665 670 675	2251
tgc tac agg att cca gcg gct cct tcc tgc agc cag agg tgg aca cct Cys Tyr Arg Ile Pro Ala Ala Pro Ser Cys Ser Gln Arg Trp Thr Pro 680 685 690 695	2299
acc ggc cgt tcc agg gca cca tgg ggg tct gtc ctc cct ccc cac cca Thr Gly Arg Ser Arg Ala Pro Trp Gly Ser Val Leu Pro Pro His Pro 700 705 710	2347
cca tat gct cca ggg ccc caa ctg caa agt tgg cca ctg agg agc cac Pro Tyr Ala Pro Gly Pro Gln Leu Gln Ser Trp Pro Leu Arg Ser His 715 720 725	2395

ctc ctc gct ooc ctc ctg agt ctg aga gtg aac ogt aca oct tct ooc 2443
 Leu Leu Ala Pro Leu Leu Ser Leu Arg Val Asn Arg Thr Pro Ser Pro
 730 735 740

atc oca aca atg ggg atg taa gcagcaagga cacagacatt occttactga 2494
 Ile Pro Thr Met Gly Met
 745 750

acactcagga gccatggag ccagcagaat aacttgatcc attccagacg ctttgctgag 2554
 tttcataaag cagggcactg agacacccgt cagtgttctt aaccagaaat cctaaagaag 2614
 aggaattata cagaaggaac agcaggaggt tttcctggac accgccaact tcacattgct 2674
 cagtggactc attctaaggg caagacattg aaaatgatga attccaatct ggatacagtc 2734
 atgacagctc atgtgctcct caacttaggc tgtgcggtta gccagcctgt aatgagagga 2794
 gagaggcctg agtcacctag catagggttg cagcaagccc tggattcaga gtgttaaaca 2854
 gaggcttgcc ctcttcagga caacagttcc aattccaagg agcctacctg aggtccctac 2914
 tctcactggg gtccccagga tgaaaaogac aatgtgcctt tttattatta tttatttggg 2974
 ggtcctgtgt tatttaagag atcaaatgta taaccaccta gctcttttca cctgacttag 3034
 taataactca tactaactgg tttggatgcc tgggttgtga ctctactga cogctagata 3094
 aacgtgtgcc tgtccccag gtggtgggaa taatttaca tctgtccaac cagaaaagaa 3154
 tgtgtgtgtt tgagcagcat tgacacatat ctgctttgat aagagacttc ctgattctct 3214
 aggtcgggtc gtggttatcc cattgtggaa attcatcttg aatccattg tctatagtc 3274
 ctagcaataa gagaaatttc ctcaagtttc catgtgcggt tctcctagct gcagcaatac 3334
 tttgacattt aaagagaaat ttagagaata ttctcatcct ctaaaaatgt ttaaataat 3394
 accaaaacagt ggccccctgc attagttttc tgttgccact gcaaccatt acttggtagc 3454
 ttaaaaaaca cacattagct tatagtctg gggatcagaa ttccaaaatg gatgtccctg 3514
 aatgaaaatc aaggtgtcag cagagctgtg ctcccttctga aggtcttagg gagaagcgg 3574
 ttccttgcca tttcaagctt ctagaggctg gctgcattcc caggctccag tggctggtca 3634
 agcttttctc acatggcatc actgtgacac tggcctccc acttccctct ttgacttaca 3694
 aagcccacca ggaagatcca ggataatctc tccatctaaa gatccttcat catcctggaa 3754
 gagccttttg ccatgcaaga caacatagcc acaggtgggg attaggacca ggacatcttt 3814
 ggggtgctgt tattctgcct accacaacct cctgccabg actccacag gagaggctac 3874
 aaaatgatct ggccacaggt gatgttttgt ttagcttgog gactctaaca cttaaaaaa 3934
 cccagatca gaagatctgg ccagtctggg gctcacattc tcacctagca acaactggct 3994

ggagctgggc accagctctg cctttagaag ggggtgtcac ttcaccaggt caccacagcc 4054
 cactactacgc cctatcactt ccacacatga ggctaagtgt ttgtttctac tgatcaatgc 4114
 ccctgcaggt tgcatttatt gtaatgaaaa agaaagactg ggattaatct ctaatcaggt 4174
 gagtagacca tgagaccaat gtgtgtcac attaccttt ttcttttttt tctttttctt 4234
 tttctttttt tttttaatgt gagacaggat ctcatctgt tgcttaggct ggagtgcagt 4294
 ggcgcaatct cggctcactg caacctctgc ctctgggct caagcaattc tccacctca 4354
 gcctcccaaa tagctgggat cactggcaca aaccacatg ccagctaatt tttgtatttt 4414
 ttgtagagac agggtttcac catgttgccc aggtgtgtct caacctctg ggctcaagca 4474
 atctctctgc ctggcctcc caaagtgtg ggattacaga tgtgagccac cgcattccagc 4534
 cccacacct cttttatacc aattacctgc ccagtaactg tggacttttg ctctctcacc 4594
 cctgctctga tctggaagga gagggattat gttatagctt gtcagcacag toccaagttc 4654
 aatattttctg cggcaaaaac ttccttcaaa aaataaatgt acttcattgt attcaatgaa 4714
 ttcaccttg aaatgcacog cctcaacttg ttcacatggc ataaatgaaa ggaattttat 4774
 agtctctaa atggcgtgta ctgcaagacc tcttgaacac ttocagagg ataggatatt 4834
 taagtcatgc ccttggcgtt gcctatggca cctttccctt ctgaaagtct ggttctgccc 4894
 cagtgaacct tggccttgtg agcagagatg ctgacctgc ataaagggcc aaaggagggc 4954
 tgcggtctcc ttccctcact gaagagocct tatttgaatt cactgtgtgg agccctagcc 5014
 ctccattctc gacattcccc aacctccag ccccttcaa gcaggactag gtgcctgca 5074
 ttccacccaa ggtgggattg gccttctta ggctggctac ttgtcaccat caccgacatc 5134
 actgttgct gcaaggacac cacgtggcca ttttcttca actgagggct caaaactct 5194
 ggacaagttg ctggctcctg agaccagtat ttctggagm tgtgcctcag tgaaggggcc 5254
 cagcctgagg aacctggct cttttctta aagcccaggc ccacttaca taaaacattt 5314
 cagggtcact ggaaacagtg aagtgccatt tgtngaagcc tactgnatgc cagccactg 5374
 ctcatccagc tggatgcca tgcctaogag gaaggccagc gcatgcagga ntggctctca 5434
 atgntgtggt cattgcacag aagggaaggt tctcaaggaa gactcaactg ggacaagcac 5494
 aagccacccg gacatggcct tggtaaaggt tagcagactg gtgtgtgtgg atctgcagt 5554
 ctctactgga aataatttat tcattgcaga tacttttttag gtggcatttt attcatttcc 5614
 tgtgctttaa ataaacaaat gtacaaaaa acaagtatca agctgtttaa gtgcttcggc 5674
 tacttgctcc ctggttcagt agaggcccc gtttccagt tgttgactgt gacaggctca 5734

gcatgggctc agcagatgct gtcttaattt gtggatgata cagaaagcca ggctttggga 5794
 tacaagttct ttctcttca ttgatgcog tgcactgtgt gaagcagatg tttttgtcog 5854
 gaaataaaaa taatagtctt ggagtctcgc caaaaaaaaa aa 5896

<210> 2
 <211> 749
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe Ser Cys
 1 5 10 15
 Gln Ser Pro Glu Asn His Phe Val Ile Glu Ile Gln Lys Asn Ile Asp
 20 25 30
 Cys Met Ser Gly Pro Cys Pro Phe Gly Glu Val Gln Leu Gln Pro Ser
 35 40 45
 Thr Ser Leu Leu Pro Thr Leu Asn Arg Thr Phe Ile Trp Asp Val Lys
 50 55 60
 Ala His Lys Ser Ile Gly Leu Glu Leu Gln Phe Ser Ile Pro Arg Leu
 65 70 75 80
 Arg Gln Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr His Ser
 85 90 95
 Ile Ser Gly Arg Ile Asp Ala Thr Val Val Arg Ile Gly Thr Phe Cys
 100 105 110
 Ser Asn Gly Thr Val Ser Arg Ile Lys Met Gln Glu Gly Val Lys Met
 115 120 125
 Ala Leu His Leu Pro Trp Phe His Pro Arg Asn Val Ser Gly Phe Ser
 130 135 140
 Ile Ala Asn Arg Ser Ser Ile Lys Arg Leu Cys Ile Ile Glu Ser Val
 145 150 155 160
 Phe Glu Gly Glu Gly Ser Ala Thr Leu Met Ser Ala Asn Tyr Pro Glu
 165 170 175
 Gly Phe Pro Glu Asp Glu Leu Met Thr Trp Gln Phe Val Val Pro Ala
 180 185 190
 His Leu Arg Ala Ser Val Ser Phe Leu Asn Phe Asn Leu Ser Asn Cys
 195 200 205
 Glu Arg Lys Glu Glu Arg Val Glu Tyr Tyr Ile Pro Gly Ser Thr Thr
 210 215 220
 Asn Pro Glu Val Phe Lys Leu Glu Asp Lys Gln Pro Gly Asn Met Ala
 225 230 235 240

Gly Asn Phe Asn Leu Ser Leu Gln Gly Cys Asp Gln Asp Ala Gln Ser
 245 250 255
 Pro Gly Ile Leu Arg Leu Gln Phe Gln Val Leu Val Gln His Pro Gln
 260 265 270
 Asn Glu Ser Asn Lys Ile Tyr Val Val Asp Leu Ser Asn Glu Arg Ala
 275 280 285
 Met Ser Leu Thr Ile Glu Pro Arg Pro Val Lys Gln Ser Arg Lys Phe
 290 295 300
 Val Pro Gly Cys Phe Val Cys Leu Glu Ser Arg Thr Cys Ser Ser Asn
 305 310 315 320
 Leu Thr Leu Thr Ser Gly Ser Lys His Lys Ile Ser Phe Leu Cys Asp
 325 330 335
 Asp Leu Thr Arg Leu Trp Met Asn Val Glu Lys Thr Ile Ser Cys Thr
 340 345 350
 Asp His Arg Tyr Cys Gln Arg Lys Ser Tyr Ser Leu Gln Val Pro Ser
 355 360 365
 Asp Ile Leu His Leu Pro Val Glu Leu His Asp Phe Ser Trp Lys Leu
 370 375 380
 Leu Val Pro Lys Asp Arg Leu Ser Leu Val Leu Val Pro Ala Gln Lys
 385 390 395 400
 Leu Gln Gln His Thr His Glu Lys Pro Cys Asn Thr Ser Phe Ser Tyr
 405 410 415
 Leu Val Ala Ser Ala Ile Pro Ser Gln Asp Leu Tyr Phe Gly Ser Phe
 420 425 430
 Cys Pro Gly Gly Ser Ile Lys Gln Ile Gln Val Lys Gln Asn Ile Ser
 435 440 445
 Val Thr Leu Arg Thr Phe Ala Pro Ser Phe Gln Gln Glu Ala Ser Arg
 450 455 460
 Gln Gly Leu Thr Val Ser Phe Ile Pro Tyr Phe Lys Glu Glu Gly Val
 465 470 475 480
 Phe Thr Val Thr Pro Asp Thr Lys Ser Lys Val Tyr Leu Arg Thr Pro
 485 490 495
 Asn Trp Asp Arg Gly Leu Pro Ser Leu Thr Ser Val Ser Trp Asn Ile
 500 505 510
 Ser Val Pro Arg Asp Gln Val Ala Cys Leu Thr Phe Phe Lys Glu Arg
 515 520 525
 Ser Gly Val Val Cys Gln Thr Gly Arg Ala Phe Met Ile Ile Gln Glu
 530 535 540

Gln Arg Thr Arg Ala Glu Glu Ile Phe Ser Leu Asp Glu Asp Val Leu
 545 550 555 560
 Pro Lys Pro Ser Phe His His His Ser Phe Trp Val Asn Ile Ser Asn
 565 570 575
 Cys Ser Pro Thr Ser Gly Lys Gln Leu Asp Leu Leu Phe Ser Val Thr
 580 585 590
 Leu Thr Pro Arg Thr Val Asp Leu Thr Val Ile Leu Ile Ala Ala Val
 595 600 605
 Gly Gly Gly Val Leu Leu Leu Ser Ala Leu Gly Leu Ile Ile Cys Cys
 610 615 620
 Val Lys Lys Lys Lys Lys Lys Thr Asn Lys Gly Pro Ala Val Gly Ile
 625 630 635 640
 Tyr Asn Gly Asn Ile Asn Thr Glu Met Pro Gly Ser Gln Lys Ser Phe
 645 650 655
 Arg Lys Gly Glu Arg Thr Met Thr Pro Met Cys Met Gln Ser Ser Arg
 660 665 670
 Thr Pro Trp Tyr Met Gly Ile Cys Tyr Arg Ile Pro Ala Ala Pro Ser
 675 680 685
 Cys Ser Gln Arg Trp Thr Pro Thr Gly Arg Ser Arg Ala Pro Trp Gly
 690 695 700
 Ser Val Leu Pro Pro His Pro Pro Tyr Ala Pro Gly Pro Gln Leu Gln
 705 710 715 720
 Ser Trp Pro Leu Arg Ser His Leu Leu Ala Pro Leu Leu Ser Leu Arg
 725 730 735
 Val Asn Arg Thr Pro Ser Pro Ile Pro Thr Met Gly Met
 740 745

<210> 3
 <211> 23
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 3
 accgcctcaa cttgttcaca tgg

<210> 4
 <211> 26
 <212> DNA
 <213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 4

ctggtctcag gagccagcaa cttgtc

26

<210> 5

<211> 25

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 5

ctcatgacgt ggcagtttgt cgttc

25

<210> 6

<211> 26

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 6

ggctcgctca ttactcaagt caacca

26

<210> 7

<211> 36

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 7

attcgcgact gatgatcgat tttttttttt tttttt

36

<210> 8

<211> 20

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 8

attcgcgact gatgatcgat

20

<210> 9
 <211> 20
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 9
 gagatattag aattctactc 20

<210> 10
 <211> 17
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 10
 gagtagaatt ctaatat 17

<210> 11
 <211> 22
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 11
 agtccatgtg aacaagttga gg 22

<210> 12
 <211> 20
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 12
 aattctocca cctcagcctc 20

<210> 13
 <211> 22
 <212> DNA
 <213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 13

aggatgaaaa cgacaatgtg cc

22

<210> 14

<211> 21

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 14

agaattgctt gagcccagga g

21

<210> 15

<211> 21

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 15

caacttcaca ttgctcagtg g

21

<210> 16

<211> 25

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 16

tgagcaagtt cagcctgggtt aagtc

25

<210> 17

<211> 26

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 17

cacogaatac tcataaagaa ggtccc

26

<210> 18
 <211> 26
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 18
 tagacttcga gcaggagatg gccact 26

<210> 19
 <211> 20
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 19
 ccagccatgt acgtagccat 20

<210> 20
 <211> 19
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 20
 ccaagaagga aggctggaa 19

<210> 21
 <211> 25
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 21
 ccatcaccat cttccaggag cgaga 25

<210> 22
 <211> 19
 <212> DNA
 <213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 22

ccaagaagga aggctggaa

19

<210> 23

<211> 20

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 23

tgcaggaggc attgctgatg

20

<210> 24

<211> 19

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 24

aaatcgtgca cttgcaggc

19

<210> 25

<211> 18

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 25

ttgatgcgtt ccagctga

18

<210> 26

<211> 21

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: Primer

<400> 26

ttgaattcac tgtgtggagc c

21

<210> 27
<211> 19
<212> DNA
<213> Synthetic sequence

<220>
<223> Description of the synthetic sequence: Primer

<400> 27
tgcaggcaac agtgatgtc 19

<210> 28
<211> 24
<212> DNA
<213> Synthetic sequence

<220>
<223> Description of the synthetic sequence: Primer

<400> 28
attggccttc cttaggctgg ctac 24

<210> 29
<211> 43
<212> DNA
<213> Synthetic sequence

<220>
<223> Description of the synthetic sequence: Primer

<400> 29
tgtagcgtga agacgacaga aagggcgtgg taccgagctc gag 43

<210> 30
<211> 22
<212> DNA
<213> Synthetic sequence

<220>
<223> Description of the synthetic sequence: Primer

<400> 30
agggcgtggt accgagctcg ag 22

<210> 31
<211> 11
<212> DNA
<213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<210> 31
 agct c

11

<210> 32
 <211> 22
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 32
 ggccatgtcc ggtgggcttg tg

22

<210> 33
 <211> 26
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 33
 ctcaaaactc ctggacaagt tgctgg

26

<210> 34
 <211> 22
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 34
 aaggtgaagg tcggagtcaa cg

22

<210> 35
 <211> 24
 <212> DNA
 <213> Synthetic sequence

<220>
 <223> Description of the synthetic sequence: Primer

<400> 35
 ggcagagatg atgacccttt tggc

24